

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, Yi
- (ii) TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPerfect 5.1, Dos Text File
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/466,343
 - (B) FILING DATE: 6 JUN 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: MULLINS, J.G.
 - (B) REGISTRATION NUMBER: 33,073
 - (C) REFERENCE/DOCKET NUMBER: 325800-449
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
 - (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1414 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60
GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTTCA TTGCTTGGCC CAAAAGAGAG 120

TTAATTCAAT GTAGACATCT ATGTAGGCAA TTA AAAACCT ATTGATGTAT AAAACAGTTT 180
GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTATTTA 240
TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339
Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387
Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435
Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln
AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483
Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579
Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr
TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627
Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr
ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723
Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771
Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
GAA GGT CTT CAT TAC ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT 819
Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867
Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915
Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963
Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011
Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059
Asn Ile Val Leu Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107
Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155
Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC 1203
Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His

C1
cont.

ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT 1251
Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala

CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA 1299
Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu

ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG 1354
Ile Ser Val Gly Leu

TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT 1414

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 352 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr
5 10 15
Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala
20 25 30
Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe
35 40 45
Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg
50 55 60
Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
65 70 75
Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala
80 85 90
Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly
95 100 105
Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln
110 115 120
Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
125 130 135
Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val
140 145 150
Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile
155 160 165

Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser
 170 175 180
 His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr
 185 190 195
 Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met
 200 205 210
 Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg
 215 220 225
 Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
 230 235 240
 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu
 245 250 255
 Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser
 260 265 270
 Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu
 275 280 285
 Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val
 290 295 300
 Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His
 305 310 315
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu
 320 325 330
 Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu
 335 340 345
 Gln Glu Ile Ser Val Gly Leu
 350

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 30 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 29 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCACAAGCC CACAGATAT

29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 34 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCAAGCTT GCCACCATGG ATTATCAAGT GTCA

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 61 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCACAAGCCC ACAGATATTT 60

C

61

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGATCCCT CCATGGATTA TCAAGTGTCA

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 29 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGATCCCG CTCACAAGCC CACAGATAT

29

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
5 10 15
His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro
20 25 30
Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu
35 40 45
Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr
50 55 60
Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu
65 70 75
Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val
80 85 90
Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile
95 100 105

Gly	Tyr	Phe	Gly	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp
			110						115					120
Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg
			125						130					135
Thr	Val	Thr	Phe	Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Leu	Val
			140						145					150
Ala	Val	Phe	Ala	Ser	Val	Pro	Gly	Ile	Ile	Phe	Thr	Lys	Cys	Gln
			155						160					165
Lys	Glu	Asp	Ser	Val	Tyr	Val	Cys	Gly	Pro	Tyr	Phe	Pro	Arg	Gly
			170						175					180
Trp	Asn	Asn	Phe	His	Thr	Ile	Met	Arg	Asn	Ile	Leu	Gly	Leu	Val
			185						190					195
Leu	Pro	Leu	Leu	Ile	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys
			200						205					210
Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val
			215						220					225
Arg	Val	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Thr
			230						235					240
Pro	Tyr	Asn	Ile	Val	Ile	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe
			245						250					255
Gly	Leu	Ser	Asn	Cys	Glu	Ser	Thr	Ser	Gln	Leu	Asp	Gln	Ala	Thr
			260						265					270
Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro
			275						280					285
Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	Ser	Leu	Phe	His
			290						295					300
Ile	Ala	Leu	Gly	Cys	Arg	Ile	Ala	Pro	Leu	Gln	Lys	Pro	Val	Cys
			305						310					315
Gly	Gly	Pro	Gly	Val	Arg	Pro	Gly	Lys	Asn	Val	Lys	Val	Thr	Thr
			320						325					330
Gln	Gly	Leu	Leu	Asp	Gly	Arg	Gly	Lys	Gly	Lys	Ser	Ile	Gly	
			335						340					

C' word